

## WEST Search History

DATE: Tuesday, February 01, 2005

Hide? Set Name Query Hit Count

*DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ*

<input type="checkbox"/>	L11	l10 and 392	2
<input type="checkbox"/>	L10	L9 and l6	9
<input type="checkbox"/>	L9	L8 and l5	13
<input type="checkbox"/>	L8	(530/387.1,387.7,388.1)![CCLS]	3884
<input type="checkbox"/>	L7	L6 and l5	139
<input type="checkbox"/>	L6	antibod\$.clm.	36182
<input type="checkbox"/>	L5	L4 or l3 or l1	13182
<input type="checkbox"/>	L4	algate.in.	25
<input type="checkbox"/>	L3	king.in.	13071
<input type="checkbox"/>	L2	king.in.L1	0
<input type="checkbox"/>	L1	Mitcham.in.	98

END OF SEARCH HISTORY

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 25, 2005, 11:36:37 ; Search time 157 Seconds  
(without alignments)  
706.034 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1574	100.0	309	3	AAB12556	Aab12556 Human ova
2	1574	100.0	309	4	AAB99205	Aab99205 Human ova
3	1574	100.0	309	5	ABP30900	Abp30900 O8E prote
4	1574	100.0	309	7	ADA08545	Ada08545 Human ova
5	1574	100.0	309	7	ADF08888	Adf08888 Secreted
6	1574	100.0	309	7	ADG46175	Adg46175 Human ova
7	1574	100.0	309	8	ADN40454	Adn40454 Human bre
8	1538	97.7	306	8	ADH50895	Adh50895 Breast an
9	1513	96.1	336	8	ADH50894	Adh50894 Breast an

10	1431	90.9	282	3	AAY66719	Aay66719 Membrane-
11	1431	90.9	282	3	AAB12557	Aab12557 Human ova
12	1431	90.9	282	4	AAU29132	Aau29132 Human PRO
13	1431	90.9	282	4	AAB87555	Aab87555 Human PRO
14	1431	90.9	282	4	AAB99204	Aab99204 Human ova
15	1431	90.9	282	4	AAB65242	Aab65242 Human PRO
16	1431	90.9	282	5	AAE20311	Aae20311 Human B7-
17	1431	90.9	282	5	ABG96445	Abg96445 Human ova
18	1431	90.9	282	5	AAU77766	Aau77766 Tumour as
19	1431	90.9	282	5	ABG95880	Abg95880 Human sec
20	1431	90.9	282	5	AAU76536	Aau76536 Tumour-as
21	1431	90.9	282	5	ABP30901	Abp30901 O8E prote
22	1431	90.9	282	5	ABB76274	Abb76274 Breast BS
23	1431	90.9	282	5	AAE18336	Aae18336 Human B7-
24	1431	90.9	282	5	ABB09879	Abb09879 Amino aci
25	1431	90.9	282	5	AAE19013	Aae19013 Human B7-
26	1431	90.9	282	6	ABU58508	Abu58508 Human PRO
27	1431	90.9	282	6	ABU88056	Abu88056 Novel hum
28	1431	90.9	282	6	ABU84371	Abu84371 Human sec
29	1431	90.9	282	6	ABR66245	Abr66245 Human sec
30	1431	90.9	282	6	ABR65635	Abr65635 Human sec
31	1431	90.9	282	6	ABU99575	Abu99575 Human sec
32	1431	90.9	282	6	ABU58057	Abu58057 Human PRO
33	1431	90.9	282	6	ABU59135	Abu59135 Novel hum
34	1431	90.9	282	6	ABU82647	Abu82647 Human sec
35	1431	90.9	282	6	ABU82814	Abu82814 Human PRO
36	1431	90.9	282	6	ABU89935	Abu89935 Novel hum
37	1431	90.9	282	6	ABR68184	Abr68184 Human sec
38	1431	90.9	282	6	ABU60566	Abu60566 Human sec
39	1431	90.9	282	6	ABU96237	Abu96237 Novel hum
40	1431	90.9	282	6	ABU92668	Abu92668 Human sec
41	1431	90.9	282	6	ABO08745	Abo08745 Human sec
42	1431	90.9	282	6	ABO02797	Abo02797 Human sec
43	1431	90.9	282	6	ABR74951	Abr74951 Human sec
44	1431	90.9	282	6	ABR94713	Abr94713 Human sec
45	1431	90.9	282	6	ABU13948	Abu13948 Human PRO

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 27, 2005, 13:05:30 ; Search time 4800 Seconds  
(without alignments)  
3044.274 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYIMLK 309

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-

Q=/cgn2\_1/USPTO\_spool\_h/US09827271/runat\_25012005\_101614\_10300/app\_query.fasta\_1  
.455

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US09827271\_@CGN\_1\_1\_3731\_@runat\_25012005\_101614\_10300 -NCPU=6 -ICPU=3

-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

```

11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1574	100.0	2627	6	BD265002	BD265002 Compositi
2	1574	100.0	2627	6	AR238405	AR238405 Sequence
3	1574	100.0	2627	6	AR478744	AR478744 Sequence
4	1574	100.0	2627	6	AX156350	AX156350 Sequence
5	1574	100.0	2627	6	AX366624	AX366624 Sequence
6	1541	97.9	1065	6	AX375858	AX375858 Sequence
7	1541	97.9	1965	6	CQ412191	CQ412191 Sequence
8	1538	97.7	1070	9	AY346100	AY346100 Homo sapi
9	1538	97.7	1658	6	AR252569	AR252569 Sequence
10	1538	97.7	1658	6	AX092328	AX092328 Sequence
11	1538	97.7	1658	6	AX376150	AX376150 Sequence
12	1538	97.7	1658	6	AX395215	AX395215 Sequence
13	1538	97.7	1658	6	AX403403	AX403403 Sequence
14	1538	97.7	1658	6	AX468680	AX468680 Sequence
15	1538	97.7	1658	9	AY358352	AY358352 Homo sapi
16	1538	97.7	2626	6	AX375860	AX375860 Sequence
17	1532	97.3	1811	9	AK026071	AK026071 Homo sapi
18	1525	96.9	2587	6	BD235830	BD235830 A novel m
19	1522	96.7	2603	6	AX403048	AX403048 Sequence
20	1513	96.1	1190	9	BC065717	BC065717 Homo sapi
21	1488	94.5	916	9	BC074729	BC074729 Homo sapi
22	1431	90.9	849	9	AY280972	AY280972 Homo sapi
23	1388.5	88.2	2671	9	HSM808167	BX648021 Homo sapi
24	1266	80.4	1382	10	AY346099	AY346099 Mus muscu
25	1261.5	80.1	852	10	AY322147	AY322147 Mus muscu
26	1257.5	79.9	852	10	AY280973	AY280973 Mus muscu
27	1257	79.9	1343	10	BC032925	BC032925 Mus muscu
28	1202	76.4	94664	9	HSJ1025A1	AL080312 Human DNA
29	1066	67.7	6370	6	AX403051	AX403051 Sequence
30	812	51.6	548	6	CQ100653	CQ100653 Sequence
31	812	51.6	548	6	CQ139644	CQ139644 Sequence
32	812	51.6	548	6	CQ223013	CQ223013 Sequence
33	812	51.6	548	6	CQ260975	CQ260975 Sequence
34	812	51.6	548	6	CQ335117	CQ335117 Sequence
35	777	49.4	462	6	BD235842	BD235842 A novel m
36	759	48.2	456	6	AX182037	AX182037 Sequence
37	690	43.8	513	6	CQ735047	CQ735047 Sequence
38	638	40.5	406	6	BD235841	BD235841 A novel m
39	610.5	38.8	390	6	AX098101	AX098101 Sequence
c 40	603	38.3	171595	9	AL391476	AL391476 Human DNA
41	571	36.3	336	6	AX375856	AX375856 Sequence
42	540.5	34.3	218776	2	AC134291	AC134291 Rattus no
c 43	540.5	34.3	286029	2	AC110845	AC110845 Rattus no

44 535.5 34.0 199673 10 AL669872  
45 512 32.5 1463 5 BC044000

AL669872 Mouse DNA  
BC044000 Xenopus 1

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 27, 2005, 12:58:11 ; Search time 552 Seconds  
(without alignments)  
2938.535 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-

Q=/cgn2\_1/USPTO\_spool\_h/US09827271/runat\_25012005\_101614\_10291/app\_query.fasta\_1  
.455  
-DB=N\_Geneseq\_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09827271\_@CGN\_1\_1\_470\_@runat\_25012005\_101614\_10291 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_23Sep04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:  
 12: geneseqn2004s:  
 .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1574	100.0	2627	3	AAA70077	Aaa70077 Human ova
2	1574	100.0	2627	4	AAH55681	Aah55681 Human ova
3	1574	100.0	2627	6	ABN72971	Abn72971 Ovarian c
4	1574	100.0	2627	9	ADA08544	Ada08544 Human ova
5	1574	100.0	2627	10	ADF08887	Adf08887 cDNA enco
6	1574	100.0	2627	10	ADG46174	Adg46174 Human ova
7	1574	100.0	2627	12	ADN40452	Adn40452 Human bre
8	1541	97.9	1065	6	ABL56580	Abl56580 Nucleotid
9	1541	97.9	1965	5	ADL45372	Adl45372 Human ova
10	1538	97.7	1657	3	AAZ65059	Aaz65059 Membrane-
11	1538	97.7	1658	4	AAS46033	Aas46033 Human DNA
12	1538	97.7	1658	4	AAF92087	Aaf92087 Human PRO
13	1538	97.7	1658	5	AAF44205	Aaf44205 Human PRO
14	1538	97.7	1658	6	ABK11744	Abk11744 DNA encod
15	1538	97.7	1658	6	ABS74407	Abs74407 Human cDN
16	1538	97.7	1658	6	ABK11091	Abk11091 cDNA enco
17	1538	97.7	1658	8	ACA89483	Aca89483 cDNA enco
18	1538	97.7	1658	8	ACA73493	Aca73493 Human sec
19	1538	97.7	1658	8	ACA05808	Aca05808 Human sec
20	1538	97.7	1658	8	ACA66642	Aca66642 cDNA enco
21	1538	97.7	1658	8	ACA64352	Aca64352 Novel hum
22	1538	97.7	1658	8	ACA91193	Aca91193 Novel hum
23	1538	97.7	1658	8	ACD81570	Acd81570 Human cDN
24	1538	97.7	1658	8	ACF20217	Acf20217 Human sec
25	1538	97.7	1658	8	ACF19603	Acf19603 Human sec
26	1538	97.7	1658	8	ACD21891	Acd21891 Human sec
27	1538	97.7	1658	8	ACF13056	Acf13056 Human sec
28	1538	97.7	1658	8	ACD25159	Acd25159 Human sec
29	1538	97.7	1658	8	ACF00208	Acf00208 Human sec
30	1538	97.7	1658	8	ACA60392	Aca60392 Novel hum
31	1538	97.7	1658	8	ACA72265	Aca72265 Novel hum
32	1538	97.7	1658	8	ACD04789	Acd04789 Novel hum
33	1538	97.7	1658	8	ACD18250	Acd18250 Human sec
34	1538	97.7	1658	8	ACD08257	Acd08257 Human sec
35	1538	97.7	1658	8	ACA88691	Aca88691 Novel hum
36	1538	97.7	1658	8	ACA70133	Aca70133 Human sec
37	1538	97.7	1658	8	ACD12355	Acd12355 Novel hum
38	1538	97.7	1658	8	ACC74270	Acc74270 Human sec
39	1538	97.7	1658	8	ACD15898	Acd15898 Human sec
40	1538	97.7	1658	8	ACD25466	Acd25466 Novel hum
41	1538	97.7	1658	8	ACD17943	Acd17943 Human sec
42	1538	97.7	1658	8	ACC88230	Acc88230 Human sec
43	1538	97.7	1658	8	ACD21584	Acd21584 Human sec
44	1538	97.7	1658	8	ACD18651	Acd18651 Human sec
45	1538	97.7	1658	8	ACA58839	Aca58839 cDNA enco

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OM protein - protein search, using sw model

Run on: January 25, 2005, 11:45:57 ; Search time 41 Seconds  
(without alignments)  
725.146 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	219.5	13.9	526	2	A37821	butyrophilin - bov
2	211.5	13.4	526	2	S70587	butyrophilin precu
3	171.5	10.9	487	2	S65133	butyrophilin - mou
4	168.5	10.7	391	2	T09058	butyrophilin homol
5	163.5	10.4	299	2	I46690	CD80 precursor - r
6	153	9.7	275	2	JC7604	CD86 spliced varia
7	151	9.6	339	2	T28138	Ig V-region-like B
8	150.5	9.6	340	2	T28137	Ig V-region-like B
9	150	9.5	247	2	A55717	myelin/oligodendro
10	147.5	9.4	329	1	A48754	B7-2 antigen - hum
11	147.5	9.4	330	2	I46691	CD86 precursor - r
12	147	9.3	218	2	B47712	myelin/oligodendro
13	146.5	9.3	372	2	C39371	Ig V-region-like B

14	146	9.3	398	2	A39371	Ig V-region-like B
15	144	9.1	247	2	S58394	myelin/oligodendro
16	143.5	9.1	309	2	I49522	gene B7-2 protein
17	140.5	8.9	246	2	A47712	myelin/oligodendro
18	135	8.6	761	1	IJHUNG	neural cell adhesi
19	134.5	8.5	503	2	JC5287	SHP substrate-1 pr
20	133	8.4	1091	1	IJCHNL	neural cell adhesi
21	132.5	8.4	853	1	IJBONC	neural cell adhesi
22	130.5	8.3	725	1	IJMSNG	neural cell adhesi
23	130.5	8.3	1033	2	S19247	cell adhesion prot
24	130.5	8.3	1115	1	IJMSNL	neural cell adhesi
25	128.5	8.2	858	1	IJRTNC	neural cell adhesi
26	127	8.1	946	1	A47299	ror-related recept
27	126.5	8.0	765	2	C42632	cell adhesion mole
28	126.5	8.0	812	2	B42632	cell adhesion mole
29	126.5	8.0	932	2	A42632	cell adhesion mole
30	126.5	8.0	1088	1	IJXNL	neural cell adhesi
31	125.5	8.0	1018	2	JC4211	neural adhesion pr
32	124	7.9	309	2	I49503	B-lymphocyte activ
33	123.5	7.8	725	2	JE0099	neural cell adhesi
34	123.5	7.8	5175	2	T20992	hypothetical prote
35	123.5	7.8	5198	2	T43290	hemicentin precurs
36	122.5	7.8	871	1	I48696	protein-tyrosine k
37	122.5	7.8	881	1	I48697	protein-tyrosine k
38	121.5	7.7	1612	2	T30805	duttl protein - mo
39	121	7.7	321	2	I54766	B-lymphocyte activ
40	121	7.7	365	2	JC7780	coxsackie- and ade
41	121	7.7	1091	2	S01998	contactin precurs
42	120	7.6	215	2	A57843	sodium channel bet
43	120	7.6	288	2	A45803	B-cell-restricted
44	120	7.6	333	2	A31923	amalgam protein pr
45	118	7.5	321	2	D39371	Ig V-region-like B

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 27, 2005, 18:42:38 ; Search time 3530 Seconds  
(without alignments)  
3189.767 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-  
Q=/cgn2\_1/USPTO\_spool\_h/US09827271/runat\_25012005\_101615\_10326/app\_query.fasta\_1  
.455  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09827271\_@CGN\_1\_1\_3437\_@runat\_25012005\_101615\_10326 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query			Description
			Match	Length	DB	
	1	1288	81.8	2431	3	CR603772
	2	1184	75.2	714	7	CN259813
	3	1087.5	69.1	757	4	BI454643
	4	1046	66.5	767	5	BX358434
	5	1012	64.3	604	5	BX499180
C	6	993	63.1	751	5	BM981657
	7	931	59.1	702	6	BY736335
	8	889	56.5	578	6	CD686218
	9	889	56.5	655	7	CN259811
	10	857.5	54.5	845	2	BF680206
	11	847	53.8	670	2	BB666051
	12	838	53.2	925	5	BX369964
	13	834.5	53.0	917	2	BE573890
	14	822	52.2	487	7	CN259818
	15	802	51.0	639	2	BE381883
C	16	752	47.8	595	5	BU680630
	17	735	46.7	849	9	AY405846
	18	678	43.1	849	9	AY405847
	19	643.5	40.9	658	2	BE308473
	20	632.5	40.2	852	9	AY405848
	21	624.5	39.7	487	1	AI155439
	22	503.5	32.0	932	7	CR439118
C	23	489	31.1	443	1	AI799522
	24	483	30.7	888	5	BQ734734
	25	480	30.5	847	6	CF223111
	26	479.5	30.5	792	5	BU458718
	27	476	30.2	830	4	BG172919
	28	472	30.0	714	5	BX847707
C	29	470	29.9	436	8	AQ479831
	30	462	29.4	292	1	AA333549
	31	423.5	26.9	712	5	BU471021
	32	421	26.7	380	5	BY116902
	33	419	26.6	693	4	BJ043488
	34	418	26.6	882	6	CF238625
	35	406	25.8	367	5	BY026217
	36	400	25.4	916	5	BQ731562
	37	387	24.6	679	4	BJ071648
	38	366	23.3	345	5	BY120095
	39	364	23.1	1141	3	CR729645
	40	362.5	23.0	608	1	AL676863
	41	358	22.7	341	5	BY117106
	42	357	22.7	1206	3	CR728324
	43	354	22.5	339	5	BY120008
	44	346	22.0	330	5	BY120640
	45	346	22.0	331	5	BY119734

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OM protein - protein search, using sw model

Run on: January 25, 2005, 11:37:22 ; Search time 193 Seconds  
(without alignments)  
921.196 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	1431	90.9	282	2	Q7Z7D3 homo sapien
2	1431	90.9	282	2	Aaq88718 homo sapi
3	1431	90.9	282	2	Aaq24206 homo sapi
4	1425	90.5	282	2	Q9h6b2 homo sapien
5	1261.5	80.1	283	2	Q7tph5 mus musculu
6	1257.5	79.9	283	2	Q7tsp5 mus musculu
7	1257.5	79.9	283	2	Aaq24205 mus muscu
8	1253.5	79.6	283	2	Q8k091 mus musculu
9	958	60.9	187	2	Q6p097 homo sapien
10	958	60.9	187	2	Aah65717 homo sapi
11	512	32.5	285	2	Q7zy30 xenopus lae
12	448	28.5	275	2	Q8avv1 xenopus lae
13	255.5	16.2	305	2	Q6dj75 xenopus tro
14	247	15.7	316	2	Q9bxr1 homo sapien
15	246	15.6	388	2	Q8nc34 homo sapien

16	246	15.6	493	2	Q6P5Y4	Q6p5y4 homo sapien
17	246	15.6	493	2	AAH62581	Aah62581 homo sapi
18	246	15.6	533	2	Q8NCB6	Q8ncb6 homo sapien
19	246	15.6	534	2	Q8NBI8	Q8nbi8 homo sapien
20	241	15.3	316	2	Q6UXI2	Q6uxi2 homo sapien
21	241	15.3	316	2	AAQ88709	Aaq88709 homo sapi
22	235	14.9	316	2	Q8VE98	Q8ve98 mus musculu
23	235	14.9	316	2	AAH56608	Aah56608 mus muscu
24	232	14.7	316	2	Q7TPB4	Q7tpb4 rattus norv
25	225.5	14.3	466	2	Q6UXE8	Q6uxe8 homo sapien
26	225.5	14.3	466	2	AAQ88751	Aaq88751 homo sapi
27	225	14.3	220	2	Q9NWQ6	Q9nwq6 homo sapien
28	225	14.3	414	2	Q9UM44	Q9um44 homo sapien
29	223	14.2	495	2	Q9HCY1	Q9hcy1 homo sapien
30	223	14.2	513	2	O00481	O00481 homo sapien
31	222.5	14.1	347	2	Q9H730	Q9h730 homo sapien
32	222.5	14.1	500	2	Q6UX41	Q6ux41 homo sapien
33	222.5	14.1	500	2	AAQ88887	Aaq88887 homo sapi
34	220	14.0	280	2	O73716	O73716 grus americ
35	219.5	13.9	286	2	O46535	O46535 bos taurus
36	215.5	13.7	304	2	Q9BE26	Q9be26 macaca fasc
37	215.5	13.7	526	1	BUTY_BOVIN	P18892 bos taurus
38	215.5	13.7	731	2	P78409	P78409 homo sapien
39	213.5	13.6	584	2	O00478	O00478 homo sapien
40	211.5	13.4	526	1	BUTY_HUMAN	Q13410 homo sapien
41	209.5	13.3	526	2	Q9H458	Q9h458 homo sapien
42	208.5	13.2	334	2	Q9NR44	Q9nr44 homo sapien
43	207.5	13.2	319	2	O00477	O00477 homo sapien
44	207.5	13.2	332	2	Q9BU81	Q9bu81 homo sapien
45	207.5	13.2	332	2	AAH02832	Aah02832 homo sapi

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OM protein - protein search, using sw model

Run on: January 25, 2005, 11:45:17 ; Search time 40 Seconds  
(without alignments)  
512.307 Million cell updates/sec

Title: US-09-827-271-392  
Perfect score: 1574  
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1:	/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2:	/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3:	/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4:	/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5:	/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6:	/cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description	
		Match	Length	DB	ID	
1	1574	100.0	309	4	US-09-404-879A-392	Sequence 392, App
2	1574	100.0	309	4	US-09-667-857-392	Sequence 392, App
3	1431	90.9	282	4	US-09-404-879A-393	Sequence 393, App
4	1431	90.9	282	4	US-09-667-857-393	Sequence 393, App
5	348	22.1	65	4	US-09-667-857-415	Sequence 415, App
6	247	15.7	316	4	US-09-910-174B-24	Sequence 24, Appl
7	247	15.7	316	4	US-09-620-461-24	Sequence 24, Appl
8	246	15.6	441	4	US-09-651-200-4	Sequence 4, Appli
9	246	15.6	534	4	US-09-651-200-6	Sequence 6, Appli
10	246	15.6	534	4	US-09-651-200-24	Sequence 24, Appl
11	245	15.6	340	4	US-09-651-200-2	Sequence 2, Appli

12	238.5	15.2	315	4	US-09-910-174B-28	Sequence 28, Appl
13	238.5	15.2	315	4	US-09-620-461-28	Sequence 28, Appl
14	223	14.2	513	4	US-09-910-174B-18	Sequence 18, Appl
15	223	14.2	513	4	US-09-620-461-18	Sequence 18, Appl
16	217.5	13.8	540	2	US-08-724-394A-4	Sequence 4, Appli
17	215.5	13.7	731	4	US-09-910-174B-15	Sequence 15, Appl
18	215.5	13.7	731	4	US-09-620-461-15	Sequence 15, Appl
19	213.5	13.6	584	4	US-09-910-174B-16	Sequence 16, Appl
20	213.5	13.6	584	4	US-09-620-461-16	Sequence 16, Appl
21	212.5	13.5	610	2	US-08-724-394A-5	Sequence 5, Appli
22	211.5	13.4	526	4	US-09-910-174B-9	Sequence 9, Appli
23	211.5	13.4	526	4	US-09-620-461-9	Sequence 9, Appli
24	211.5	13.4	589	2	US-08-724-394A-1	Sequence 1, Appli
25	207.5	13.2	319	4	US-09-910-174B-12	Sequence 12, Appl
26	207.5	13.2	319	4	US-09-620-461-12	Sequence 12, Appl
27	207.5	13.2	342	2	US-08-724-394A-6	Sequence 6, Appli
28	207.5	13.2	357	4	US-09-910-174B-14	Sequence 14, Appl
29	207.5	13.2	357	4	US-09-620-461-14	Sequence 14, Appl
30	204	13.0	290	4	US-09-910-174B-19	Sequence 19, Appl
31	204	13.0	290	4	US-09-620-461-19	Sequence 19, Appl
32	204	13.0	350	4	US-09-651-200-25	Sequence 25, Appl
33	204	13.0	350	4	US-09-910-174B-17	Sequence 17, Appl
34	204	13.0	350	4	US-09-620-461-17	Sequence 17, Appl
35	199.5	12.7	290	4	US-09-910-174B-32	Sequence 32, Appl
36	196	12.5	296	4	US-09-667-135-36	Sequence 36, Appl
37	193	12.3	527	4	US-09-910-174B-10	Sequence 10, Appl
38	193	12.3	527	4	US-09-620-461-10	Sequence 10, Appl
39	192	12.2	329	4	US-09-651-200-18	Sequence 18, Appl
40	192	12.2	329	4	US-09-303-040-6	Sequence 6, Appli
41	188.5	12.0	290	4	US-09-910-174B-8	Sequence 8, Appli
42	188.5	12.0	290	4	US-09-620-461-8	Sequence 8, Appli
43	186	11.8	529	4	US-09-910-174B-13	Sequence 13, Appl
44	186	11.8	529	4	US-09-620-461-13	Sequence 13, Appl
45	186	11.8	581	2	US-08-724-394A-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: January 25, 2005, 11:54:35 ; Search time 145 Seconds  
(without alignments)  
769.920 Million cell updates/sec

Title: US-09-827-271-392  
Perfect score: 1574  
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1574	100.0	309	9	US-09-778-320-209	Sequence 209, App
2	1574	100.0	309	9	US-09-910-689-209	Sequence 209, App
3	1574	100.0	309	9	US-09-884-441-392	Sequence 392, App
4	1574	100.0	309	10	US-09-907-969-392	Sequence 392, App
5	1574	100.0	309	10	US-09-827-271-392	Sequence 392, App
6	1574	100.0	309	13	US-10-010-742-209	Sequence 209, App
7	1574	100.0	309	14	US-10-198-053-392	Sequence 392, App
8	1574	100.0	309	16	US-10-714-389-209	Sequence 209, App
9	1574	100.0	309	16	US-10-717-296-209	Sequence 209, App
10	1431	90.9	282	9	US-09-778-320-208	Sequence 208, App
11	1431	90.9	282	9	US-09-850-178-33	Sequence 33, Appl
12	1431	90.9	282	9	US-09-877-065-8	Sequence 8, Appli
13	1431	90.9	282	9	US-09-989-722-291	Sequence 291, App
14	1431	90.9	282	9	US-09-989-723-291	Sequence 291, App
15	1431	90.9	282	9	US-09-989-279-291	Sequence 291, App
16	1431	90.9	282	9	US-09-989-727-291	Sequence 291, App
17	1431	90.9	282	9	US-09-910-689-208	Sequence 208, App
18	1431	90.9	282	9	US-09-989-731-291	Sequence 291, App
19	1431	90.9	282	9	US-09-884-441-393	Sequence 393, App
20	1431	90.9	282	9	US-09-989-732-291	Sequence 291, App
21	1431	90.9	282	9	US-09-991-073-291	Sequence 291, App
22	1431	90.9	282	9	US-09-990-442-291	Sequence 291, App
23	1431	90.9	282	9	US-09-991-163-291	Sequence 291, App
24	1431	90.9	282	9	US-09-993-604-291	Sequence 291, App
25	1431	90.9	282	9	US-09-990-456-291	Sequence 291, App
26	1431	90.9	282	9	US-09-989-721-291	Sequence 291, App
27	1431	90.9	282	9	US-09-992-598-291	Sequence 291, App
28	1431	90.9	282	9	US-09-896-738-2	Sequence 2, Appli
29	1431	90.9	282	9	US-09-915-789A-5	Sequence 5, Appli
30	1431	90.9	282	9	US-09-989-293A-291	Sequence 291, App
31	1431	90.9	282	9	US-09-989-735-291	Sequence 291, App
32	1431	90.9	282	9	US-09-990-444-291	Sequence 291, App
33	1431	90.9	282	9	US-09-991-181-291	Sequence 291, App
34	1431	90.9	282	9	US-09-989-730-291	Sequence 291, App
35	1431	90.9	282	9	US-09-990-436-291	Sequence 291, App
36	1431	90.9	282	9	US-09-993-687-291	Sequence 291, App
37	1431	90.9	282	10	US-09-989-734-291	Sequence 291, App
38	1431	90.9	282	10	US-09-997-653-291	Sequence 291, App
39	1431	90.9	282	10	US-09-989-724-291	Sequence 291, App
40	1431	90.9	282	10	US-09-989-728-291	Sequence 291, App
41	1431	90.9	282	10	US-09-990-441-291	Sequence 291, App
42	1431	90.9	282	10	US-09-993-667-291	Sequence 291, App
43	1431	90.9	282	10	US-09-997-428-291	Sequence 291, App
44	1431	90.9	282	10	US-09-997-666-291	Sequence 291, App
45	1431	90.9	282	10	US-09-990-438-291	Sequence 291, App

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 27, 2005, 18:59:23 ; Search time 107 Seconds  
(without alignments)  
2052.652 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool\_h/US09827271/runat\_25012005\_101615\_10354/app\_query.fasta\_1  
.455  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09827271\_@CGN\_1\_1\_69\_@runat\_25012005\_101615\_10354 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1574	100.0	2627	4	US-09-404-879A-391	Sequence 391, App
2	1574	100.0	2627	4	US-09-667-857-391	Sequence 391, App
3	1379	87.6	1046	4	US-09-799-451-332	Sequence 332, App
4	246	15.6	1323	4	US-09-651-200-9	Sequence 9, Appli
5	246	15.6	1602	4	US-09-651-200-11	Sequence 11, Appli
6	246	15.6	2229	4	US-09-651-200-5	Sequence 5, Appli
7	246	15.6	2691	4	US-09-651-200-1	Sequence 1, Appli
8	246	15.6	2885	4	US-09-651-200-3	Sequence 3, Appli
9	246	15.6	3063	4	US-09-620-312D-844	Sequence 844, App
10	245	15.6	1020	4	US-09-651-200-7	Sequence 7, Appli
11	243	15.4	951	4	US-09-910-174B-23	Sequence 23, Appli
12	243	15.4	951	4	US-09-620-461-23	Sequence 23, Appli
13	238.5	15.2	948	4	US-09-910-174B-27	Sequence 27, Appli
14	238.5	15.2	948	4	US-09-620-461-27	Sequence 27, Appli
15	223	14.2	3416	2	US-08-724-394A-15	Sequence 15, Appli
16	213.5	13.6	2926	2	US-08-724-394A-13	Sequence 13, Appli
17	213.5	13.6	2970	4	US-09-566-921-105	Sequence 105, App
18	209	13.3	1645	2	US-08-724-394A-14	Sequence 14, Appli
19	199.5	12.7	1080	4	US-09-303-040-5	Sequence 5, Appli
20	193	12.3	2882	2	US-08-724-394A-12	Sequence 12, Appli
21	188.5	12.0	873	4	US-09-910-174B-22	Sequence 22, Appli
22	188.5	12.0	873	4	US-09-620-461-22	Sequence 22, Appli
23	183	11.6	3502	2	US-08-724-394A-16	Sequence 16, Appli
24	163.5	10.4	900	4	US-09-495-052-61	Sequence 61, Appli
25	160	10.2	3479	4	US-10-140-002-123	Sequence 123, App
26	158	10.0	1163	3	US-08-479-744A-22	Sequence 22, Appli
27	158	10.0	1163	3	US-08-280-757B-22	Sequence 22, Appli
28	158	10.0	1163	4	US-09-425-762-22	Sequence 22, Appli
29	157.5	10.0	1151	2	US-08-456-104-3	Sequence 3, Appli
30	157.5	10.0	1151	3	US-08-205-697A-20	Sequence 20, Appli
31	157.5	10.0	1151	3	US-08-702-525-20	Sequence 20, Appli
32	157.5	10.0	1151	4	US-09-837-867A-20	Sequence 20, Appli
33	157.5	10.0	1151	4	US-09-206-132-3	Sequence 3, Appli
34	157.5	10.0	1151	5	PCT-US95-02576-20	Sequence 20, Appli
35	157.5	10.0	1183	4	US-09-441-411-23	Sequence 23, Appli
36	157.5	10.0	1261	3	US-08-205-697A-12	Sequence 12, Appli
37	157.5	10.0	1261	3	US-08-702-525-12	Sequence 12, Appli
38	157.5	10.0	1261	4	US-09-837-867A-12	Sequence 12, Appli
39	157.5	10.0	1261	5	PCT-US95-02576-12	Sequence 12, Appli
40	154	9.8	1424	3	US-09-326-186B-226	Sequence 226, App
41	154	9.8	1424	4	US-09-441-411-21	Sequence 21, Appli
42	154	9.8	1428	5	PCT-US94-09642-1	Sequence 1, Appli
43	149.5	9.5	1161	3	US-08-205-697A-24	Sequence 24, Appli
44	149.5	9.5	1161	3	US-08-702-525-24	Sequence 24, Appli
45	149.5	9.5	1161	4	US-09-837-867A-24	Sequence 24, Appli

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 27, 2005, 21:14:25 ; Search time 624 Seconds  
(without alignments)  
2845.320 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574

Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFFAISWALLPLSPYLMNK 309

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-  
Q=/cgn2\_1/USPTO\_spool\_h/US09827271/runat\_25012005\_101618\_10496/app\_query.fasta\_1  
.455  
-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09827271\_@CGN\_1\_1\_480\_@runat\_25012005\_101618\_10496  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

```

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	1574	100.0	2627	9	US-09-778-320-207	Sequence 207, App
2	1574	100.0	2627	9	US-09-910-689-207	Sequence 207, App
3	1574	100.0	2627	9	US-09-884-441-391	Sequence 391, App
4	1574	100.0	2627	10	US-09-907-969-391	Sequence 391, App
5	1574	100.0	2627	10	US-09-827-271-391	Sequence 391, App
6	1574	100.0	2627	13	US-10-010-742-207	Sequence 207, App
7	1574	100.0	2627	15	US-10-198-053-391	Sequence 391, App
8	1574	100.0	2627	17	US-10-714-389-207	Sequence 207, App
9	1574	100.0	2627	17	US-10-717-296-207	Sequence 207, App
10	1541	97.9	1065	9	US-09-877-065-5	Sequence 5, Appli
11	1541	97.9	1965	10	US-09-814-353-19262	Sequence 19262, A
12	1538	97.7	1658	9	US-09-989-722-290	Sequence 290, App
13	1538	97.7	1658	9	US-09-989-723-290	Sequence 290, App
14	1538	97.7	1658	9	US-09-989-279-290	Sequence 290, App
15	1538	97.7	1658	9	US-09-989-727-290	Sequence 290, App
16	1538	97.7	1658	9	US-09-989-731-290	Sequence 290, App
17	1538	97.7	1658	9	US-09-989-732-290	Sequence 290, App
18	1538	97.7	1658	9	US-09-991-073-290	Sequence 290, App
19	1538	97.7	1658	9	US-09-990-442-290	Sequence 290, App
20	1538	97.7	1658	9	US-09-991-163-290	Sequence 290, App
21	1538	97.7	1658	9	US-09-993-604-290	Sequence 290, App
22	1538	97.7	1658	9	US-09-990-456-290	Sequence 290, App
23	1538	97.7	1658	9	US-09-989-721-290	Sequence 290, App
24	1538	97.7	1658	9	US-09-992-598-290	Sequence 290, App
25	1538	97.7	1658	9	US-09-989-293A-290	Sequence 290, App
26	1538	97.7	1658	9	US-09-989-735-290	Sequence 290, App
27	1538	97.7	1658	9	US-09-990-444-290	Sequence 290, App
28	1538	97.7	1658	9	US-09-991-181-290	Sequence 290, App
29	1538	97.7	1658	9	US-09-989-730-290	Sequence 290, App
30	1538	97.7	1658	9	US-09-990-436-290	Sequence 290, App
31	1538	97.7	1658	9	US-09-993-687-290	Sequence 290, App
32	1538	97.7	1658	10	US-09-989-734-290	Sequence 290, App
33	1538	97.7	1658	10	US-09-997-653-290	Sequence 290, App
34	1538	97.7	1658	10	US-09-989-724-290	Sequence 290, App
35	1538	97.7	1658	10	US-09-989-728-290	Sequence 290, App
36	1538	97.7	1658	10	US-09-990-441-290	Sequence 290, App

37	1538	97.7	1658	10	US-09-993-667-290	Sequence 290, App
38	1538	97.7	1658	10	US-09-997-428-290	Sequence 290, App
39	1538	97.7	1658	10	US-09-997-666-290	Sequence 290, App
40	1538	97.7	1658	10	US-09-990-438-290	Sequence 290, App
41	1538	97.7	1658	10	US-09-990-562-290	Sequence 290, App
42	1538	97.7	1658	10	US-09-990-711-290	Sequence 290, App
43	1538	97.7	1658	10	US-09-989-726-290	Sequence 290, App
44	1538	97.7	1658	10	US-09-998-156-290	Sequence 290, App
45	1538	97.7	1658	10	US-09-990-437-290	Sequence 290, App